Monia T. Russo

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Current Position: VI CTER

Current Affiliation: Sezione RIMAR Unità MB&BI Stazione Zoologica Anton Dohrn

Education/Training/Experience

Institute and Location	Degree / Function	Year	Field of Study
Department of Developmental and Molecular Biology, Stazione Zoologica A. Dohrn, Napoli, Italy	Master (Laurea)	1998-2000	Biological Sciences
Department of Developmental and Molecular Biology, Stazione Zoologica A. Dohrn, Napoli, Italy	Ph.D.	2000-2005	Molecular Genetics of Development and Differentiation
Department of Developmental and Molecular Biology, Stazione Zoologica A. Dohrn, Napoli, Italy	Postdoc	2006-2008	Nervous System Development in Ascidians
Department of Biochemistry e Medical Biotechnologies CEINGE Biotecnologie Avanzate, Napoli, Italy	Postdoc	2009	Regulation of gene expression in development and skin diseases
Integrative Marine Ecology Department Stazione Zoologica A. Dohrn Napoli, Italy	Postdoc	2010-2019	Genetics, molecular biology and mutagenesis in marine algae
MB&BI Unit, RIMAR Department Stazione Zoologica A. Dohrn Napoli, Italy	Technical collaborator	2019	Molecular biology, gene expression and mutagenesis

Publications

Author of 14 publications on ISI-journals

Aniello, F., Villano, G., Corrado, M., Locascio, A., **Russo, M. T.**, D'Aniello, S., Fucci, L., Branno, M. (2003). Structural organization of the sea urchin DNA (cytosine-5)-methyltransferase gene and characterization of five alternative spliced transcripts. Gene 302 1-9. WOS:000180682700001.

Russo, M. T., Donizetti, A., Locascio, A., D'Aniello, S., Amoroso, A., Aniello, F., Fucci, L., Branno, M. (2004). Regulatory Elements Controlling *Ci-msx*b Tissue Specific Expression during *Ciona intestinalis* embryonic development. Dev Biol 267 517-18. WOS:000220351400018.

D'Aniello, S., D'Aniello, E., Locascio, A., Memoli, A., Corrado, M., **Russo, M.T.**, Aniello, F., Fucci, L., Brown, E. R. and Branno, M. (2006). The ascidian homologue of the vertebrate homeobox gene *Rx* is essential for ocellus development and function. Differentiation 74 222-34. WOS:000237811900003.

Alfano, C., **Russo, M. T.**, Spagnuolo, A. (2007). Developmental expression and transcriptional regulation of Ci-Pans, a novel neural marker gene of the ascidian *Ciona intestinalis*. Gene 406 36-41. WOS:000252500500006. **Co-first authorship**

Sordino, P., Andreakis, N., Brown, E. R., Leccia, N. I., Squarzoni, P., Tarallo R., Alfano, C., Caputi, L., D'Ambrosio, P., Daniele, P., D'Aniello, E., D'Aniello, S., Maiella, S., Miraglia, V., **Russo, M.T.**, Sorrenti, G., Branno, M., Cariello, L., Cirino, P., Locascio, A., Spagnuolo, A., Zanetti, L. and Ristoratore, F. (2008). Natural Variation of Model Mutant Phenotypes in *Ciona intestinalis*. PLoS ONE 3(6): e2344. doi:10.1371/journal.pone.0002344. WOS:000262614300037.

De Rosa, L., Antonini, D., Ferone, G., **Russo, M.T.,** Yu, P. B., Han, R. and Missero, C. (2009). p63 suppresses non-epidermal gene expression by direct regulation of BMP/Smad signaling. J Biol Chem. 284 30574-82. WOS:000271090000060.

Antonini, D., **Russo, M.T.,** De Rosa, L., Gorrese, M., Del Vecchio, L., and Missero, C. (2010). Transcriptional repression of miR-34 family contributes to p63-mediated cell cycle progression in epidermal cells. J. Invest. Dermatol. 130(5):1249-57. WOS:000276972300010.

Russo, M.T., Racioppi, C., Zanetti, L., Ristoratore, F. (2014). Expression of a single prominin homolog in the embryo of the model chordate *Ciona intestinalis*. Gene Expr Patterns 15(1):38-45. WOS:000338610900005.

Sabatino, V., **Russo, M.T**., Patil, S., d'Ippolito, G., Fontana, A. and Ferrante, M.I. (2015). Establishment of genetic transformation in the sexually reproducing diatoms *Pseudo-nitzschia multistriata* and *Pseudo-nitzschia arenysensis* and inheritance of the transgene. Marine Biotechnology 17(4):452-462. WOS:000357122000008. **Co-first authorship**

Russo, M.T., Annunziata, R., Sanges, R., Ferrante, M.I., Falciatore, A. (2015). The upstream regulatory sequence of the light harvesting complex Lhcf2 gene of the marine diatom *Phaeodactylum tricornutum* enhances transcription in an orientation- and distance-independent fashion. Marine Genomics 24: 69–79. WOS:000367774900009. **Co-corresponding authorship**

Basu, S., Patil, S., Mapleson, D., **Russo, M.T.**, Vitale, L., Fevola, C., Maumus, F., Casotti, R., Mock, T., Caccamo, M., Montresor, M., Sanges, R., Ferrante, M.I. (2017). Finding a partner in the ocean: molecular and evolutionary bases of the response to sexual cues in a planktonic diatom. New Phytologist 215: 140–156. WOS:000402413100015.

Kroth, P.G., Bones, A.M., Daboussi, F., Ferrante, M.I., Jaubert, M., Kolot, M., Nymark, M., Río Bártulos, C., Ritter, A., **Russo, M.T.**, Serif, M., Winge, P., Falciatore, A. (2018). Genome editing in diatoms: achievements and goals. Plant cell reports 37: 1401–1408. WOS:000445435800005.

Russo, M.T., Aiese Cigliano, R., Sanseverino, W., Ferrante, M.I. (2018). Assessment of genomic changes in a CRISPR/Cas9 *Phaeodactylum tricornutum* mutant through whole genome resequencing. PeerJ 6:e5507; DOI 10.7717/peerj.5507 WOS:000447208100001 **Co-corresponding authorship.**

Russo, M.T., Vitale, L., Entrambasaguas, L., Anestis, K., Fattorini, N., Romano, F., Minucci, C., De Luca, P., Biffali, E., Vyverman, W., Sanges, R., Montresor, M., Ferrante, M.I. (2018). MRP3 is a sex determining gene in the diatom *Pseudo-nitzschia multistriata*. Nature Communications 9:5050; DOI: 10.1038/s41467-018-07496-0. WOS:000451433800020

Laboratory techniques expertise:

Molecular biology and biochemistry techniques, Southern blotting, SDS-PAGE and Western blotting, Mobility shift assay, Real time PCR, Digital PCR, DNAseq, RNAseq, cell cultures, histology, confocal microscopy, maintaining, propagation, transfection and infection of mammals cells (murine primary keratinocytes, human keratinocytes, Human Embryonic Kidney 293 cells, Squamous cell carcinoma, HeLa cells), RNA silencing, preparation of ecotropic and amphotropic viruses, nuclear transformation of tunicate eggs by electroporation, diatom transformation by biolistic and bacterial conjugation, in situ hybridization and immunohistochemistry of whole mount embryos and tissue sections, gene down-regulation by RNAi and genome editing by CRISPR/Cas9 in diatoms.

Bioinformatic skills

Familiarity with resources of sequence depository websites such as UCSC, Ensembl, JGI Genome browsers, NCBI genbank; tools for sequence analysis such as NCBI BLAST, ClustalW, Align, Serial Cloner, Vector NTI, Primer3, Oligo analyzer, Expasy; tools for CRISPR-cas9 target design and off- target finder such as CRISPOR, Cas-OFFinder, PhytoCRISP-Ex, CHOPCHOP; visualization tool for interactive exploration of large, integrated genomic datasets such as IGV.